

0 20 40
 GAAAATGGCGCCTCACGGCCCGGGTAGTCTTACGACCCTGGTGCCCTGGGCTGCCGCCCT

 CTTTTACCGCGGAGTGCCGGGCCCATCAGAATGCTGGGACCACGGGACCCGACGGCGGGA
 M A P H G P G S L T T L V P W A A A L
 60 80 100
 GCTCCTCGCTCTGGGCGTGGAAAGGGCTCTGGCGCTACCCGAGATATGCACCCAAATGTCC

 CGAGGAGCGAGACCCGCACCTTTCCCGAGACCGCGATGGGCTCTATACGTGGGTTACAGG
 L L A L G V E R A L A L P E I C T Q C P
 120 140 160
 AGGGAGCGTGCAAAATTTGTCAAAAGTGGCCTTTTATTGTAAAACGACACGAGAGCTAAT

 TCCCTCGCACGTTTTTAAACAGTTTTTACCAGGAAAATAACATTTTGCTGTGCTCTCGATTA
 G S V Q N L S K V A F Y C K T T R E L M
 180 200 220
 GCTGCATGCCCCGTTGCTGCCTGAATCAGAAGGGCACCATCTTGGGGCTGGATCTCCAGAA

 CGACGTACGGGCAACGACGGACTTAGTCTTCCCGTGGTAGAACCCCGACCTAGAGGCTCTT
 L H A R C C L N Q K G T I L G L D L Q N
 240 260 280
 CTGTTCTCTGGAGGACCCTGGTCCAAACTTTTCATCAGGCACATACCCTGTCTCATAGA

 GACAAGAGACCTCCTGGGACCAGGTTTTGAAAGTAGTCCGTGTATGGTGACAGTAGTATCT
 C S L E D P G P N F H Q A H T T V I I D
 300 320 340
 CCTGCAAGCAAACCCCTCAAAGGTGACTTGGCCAACACCTTCCGTGGCTTTACTCAGCT

 GGACGTTTCGTTTGGGGGAGTTTCCACTGAACCGGTTGTGGAAGGCACCGAAATGAGTCCA
 L Q A N P L K G D L A N T F R G F T Q L
 360 380 400
 CCAGACTCTGATACTGCCACAACATGTCAACTGTCCTGGAGGAATTAATGCCTGGAATAC

 GGTCTGAGACTATGACGGTGTGTACAGTTGACAGGACCTCCTTAATTACGGACCTTATG
 Q T L I L P Q H V N C P G G I N A W N T
 420 440 460
 TATCACCTCTTATATAGACAACCAATCTGTCAAGGGCAAAGAACCTTTGCAATAACAC

 ATAGTGAGAGAATATATCTGTTGGTTTAGACAGTTCCCGTTTTCTTGGAACGTTATTGTG
 I T S Y I D N Q I C Q G Q K N L C N N T
 480 500 520
 TGGGGACCCAGAAATGTGTCCTGAGAATGGATCTTGTGTACCTGATGGTCCAGGTCTTTT

 ACCCCTGGGTCTTTACACAGGACTCTTACCTAGAACACATGGACTACCAGGTCCAGAAAA
 G D P E M C P E N G S C V P D G P G L L
 540 560 580

FIGURE 1A

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GCAGTGTGTTTGTGCTGATGGTTTCCATGGATAACAAGTGTATGCGCCAGGGCTCGTTCTC
-----+-----+-----+-----+-----+-----+-----+-----+-----+
CGTCACACAAACACGACTACCAAAGGTACCTATGTTTACATACGCGGTCCCGAGCAAGAG
Q C V C A D G F H G Y K C M R Q G S F S
600                               620                               640

ACTGCTTATGTTCTTTCGGGATTCTGGGAGCCACCACTCTATCCGTCTCCATTCTGCTTTG
-----+-----+-----+-----+-----+-----+-----+-----+-----+
TGACGAATACAAGAAGCCCTAAGACCCTCGGTGGTGAGATAGGCAGAGGTAAGACGAAAC
L L M F F G I L G A T T L S V S I L L W
660                               680                               700

GGCGACCCAGCGCCGAAAAGCCAAGACTTCATGAACTACATAGGTCTTACCATTGACCTA
-----+-----+-----+-----+-----+-----+-----+-----+-----+
CCGCTGGGTGCGCGGCTTTTCGGTTCTGAAGTACTTGATGTATCCAGAATGGTAACCTGGAT
A T Q R R K A K T S *
720                               740                               760

AGATCAATCTGAACTATCTTAGCCCCAGTCAGGGAGCTCTGCTTCCTAGAAAGGCATCTTT
-----+-----+-----+-----+-----+-----+-----+-----+-----+
TCTAGTTAGACTTGATAGAATCGGGTCAGTCCCTCGAGACGAAGGATCTTTCCGTAGAAA
780                               800                               820

CGCCAGTGGATTCCGCTCAAGGTTGAGGCCGCCATTGGAAGATGAAAAATTGCACTCCCT
-----+-----+-----+-----+-----+-----+-----+-----+-----+
GCGGTCACCTAAGCGGAGTTCCAACCTCCGGCGGTAACCTTCTACTTTTTTAACGTGAGGGA
840                               860                               880

TGGTGTAGACAAATACCAGTTCCCATTGGTGTGTTGCCTATAATAAACACTTTTTTCTT
-----+-----+-----+-----+-----+-----+-----+-----+-----+
ACCACATCTGTTTATGGTCAAGGGTAACCACAACAACGGATATTATTTGTAAAAAAGAA
900

TTTTAAAAAAAAAAAAAAAAAAAAA
-----+-----+-----+-----+-----+-----+-----+-----+-----+
AAAATTTTTTTTTTTTTTTTTTTT

```

FIGURE 1B

Human	TGPa	VVSFHND	CPDSHTQF	-CFH-GTCRFLVQEDK	PACVCHSGYVGARCEHADLLA
TGFαH3		66	KNL	CNNNTGDP	EMCPENGSCVPDGPGLLQ-CVCADGFHGYKCMRQGSFSLIM

FIGURE 2

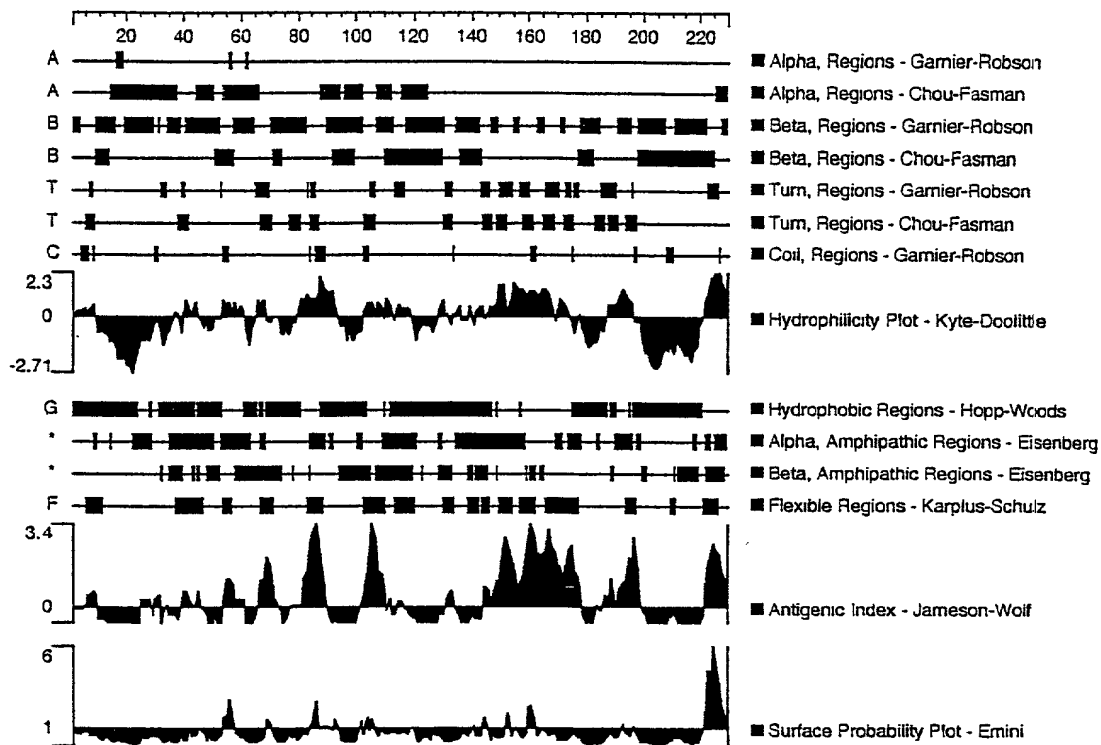


FIGURE 3

AoSMC Alamar Blue Proliferation Assay

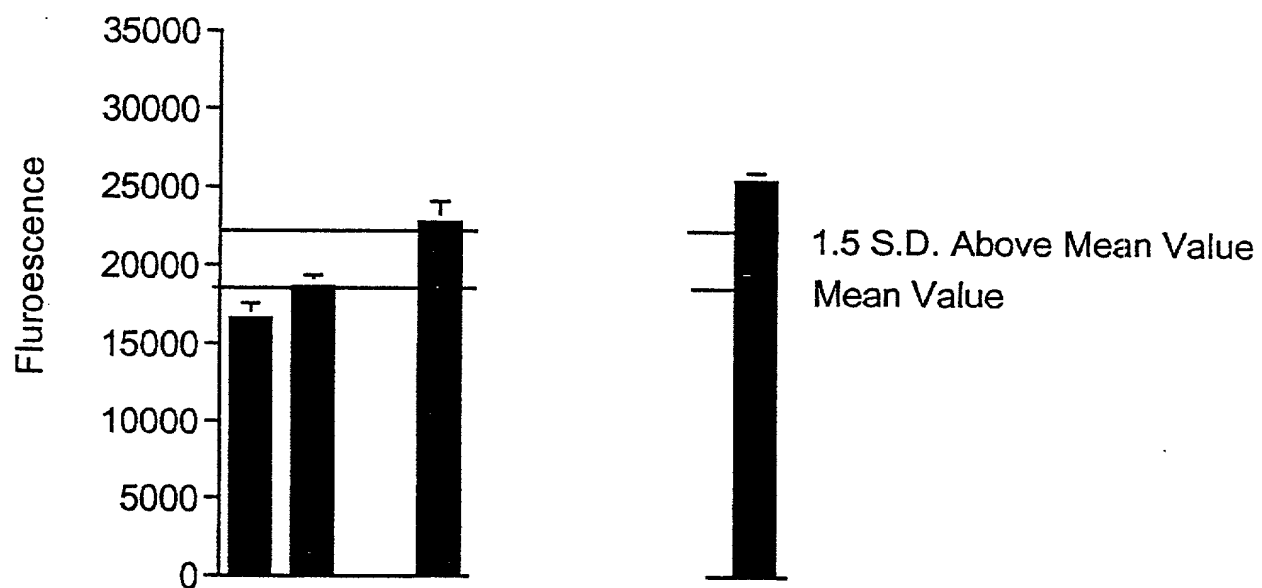


FIGURE 4